

SEQUENCE LISTING

<110> FRASER, JOHN DAVID
PROFT, THOMAS

<120> SUPERANTIGENS

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<140> 09/869,136
<141> 2001-07-20

<150> PCT/NZ99/00228
<151> 1999-12-24

<150> NZ 333589
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<170> PatentIn Ver. 2.1

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<212> DNA
<213> Streptococcus pyogenes

<220>
<221> CDS
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1	5	10	15	
ata att tct cgt cct gtg ttt gga tta gaa gta gat aat aat tcc ctt				96
Ile Ile Ser Arg Pro Val Phe Gly Leu Glu Val Asp Asn Asn Ser Leu				
20	25	30		
cta agg aat atc tat agt acg att gta tat gaa tat tca gat ata gta				144
Leu Arg Asn Ile Tyr Ser Thr Ile Val Tyr Glu Tyr Ser Asp Ile Val				
35	40	45		
att gat ttt aaa acc agt cat aac tta gtg act aag aaa ctt gat gtt				192
Ile Asp Phe Lys Thr Ser His Asn Leu Val Thr Lys Lys Leu Asp Val				
50	55	60		
aga gat gct aga gat ttc ttt att aac tcc gaa atg gac gaa tat gca				240
Arg Asp Ala Arg Asp Phe Phe Ile Asn Ser Glu Met Asp Glu Tyr Ala				
65	70	75	80	
gcc aat gat ttt aaa act gga gat aaa ata gct gtg ttc tcc gtc cca				288
Ala Asn Asp Phe Lys Thr Gly Asp Lys Ile Ala Val Phe Ser Val Pro				
85	90	95		

ttt gat tgg aac tat tta tca aaa gga aaa gtc aca gca tat acc tat Phe Asp Trp Asn Tyr Leu Ser Lys Gly Lys Val Thr Ala Tyr Thr Tyr 100 105 110	336
ggt gga ata aca ccc tac caa aaa act tca ata cct aaa aat atc cct Gly Gly Ile Thr Pro Tyr Gln Lys Thr Ser Ile Pro Lys Asn Ile Pro 115 120 125	384
gtt aat tta tgg att aat gga aag cag atc tct gtt cct tac aac gaa Val Asn Leu Trp Ile Asn Gly Lys Gln Ile Ser Val Pro Tyr Asn Glu 130 135 140	432
ata tca act aac aaa aca aca gtt aca gct caa gaa att gat cta aag Ile Ser Thr Asn Lys Thr Thr Val Thr Ala Gln Glu Ile Asp Leu Lys 145 150 155 160	480
gtt aga aaa ttt tta ata gca caa cat caa tta tat tct tct ggt tct Val Arg Lys Phe Leu Ile Ala Gln His Gln Leu Tyr Ser Ser Gly Ser 165 170 175	528
agc tac aaa agt ggt aga ctg gtt ttt cat aca aat gat aat tca gat Ser Tyr Lys Ser Gly Arg Leu Val Phe His Thr Asn Asp Asn Ser Asp 180 185 190	576
aaa tat tct ttc gat ctt ttc tat gta gga tat aga gat aaa gaa agt Lys Tyr Ser Phe Asp Leu Phe Tyr Val Gly Tyr Arg Asp Lys Glu Ser 195 200 205	624
atc ttt aaa gta tac aaa gac aat aaa tct ttc aat ata gat aaa att Ile Phe Lys Val Tyr Lys Asp Asn Lys Ser Phe Asn Ile Asp Lys Ile 210 215 220	672
ggg cat tta gat ata gaa att gac tcc taa Gly His Leu Asp Ile Glu Ile Asp Ser 225 230	702
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Ile Ile Ser Arg Pro Val Phe Gly Leu Glu Val Asp Asn Asn Ser Leu 20 25 30	
Leu Arg Asn Ile Tyr Ser Thr Ile Val Tyr Glu Tyr Ser Asp Ile Val 35 40 45	
Ile Asp Phe Lys Thr Ser His Asn Leu Val Thr Lys Lys Leu Asp Val 50 55 60	
Arg Asp Ala Arg Asp Phe Phe Ile Asn Ser Glu Met Asp Glu Tyr Ala 65 70 75 80	

Ala Asn Asp Phe Lys Thr Gly Asp Lys Ile Ala Val Phe Ser Val Pro
 85 90 95

Phe Asp Trp Asn Tyr Leu Ser Lys Gly Lys Val Thr Ala Tyr Thr Tyr
 100 105 110

Gly Gly Ile Thr Pro Tyr Gln Lys Thr Ser Ile Pro Lys Asn Ile Pro
 115 120 125

Val Asn Leu Trp Ile Asn Gly Lys Gln Ile Ser Val Pro Tyr Asn Glu
 130 135 140

Ile Ser Thr Asn Lys Thr Thr Val Thr Ala Gln Glu Ile Asp Leu Lys
 145 150 155 160

Val Arg Lys Phe Leu Ile Ala Gln His Gln Leu Tyr Ser Ser Gly Ser
 165 170 175

Ser Tyr Lys Ser Gly Arg Leu Val Phe His Thr Asn Asp Asn Ser Asp
 180 185 190

Lys Tyr Ser Phe Asp Leu Phe Tyr Val Gly Tyr Arg Asp Lys Glu Ser
 195 200 205

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 210 215 220

Gly His Leu Asp Ile Glu Ile Asp Ser
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<213> Streptococcus pyogenes

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<221> CDS

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tat gga agt caa tta gct tat gca gat gaa aat tta aaa gat tta aaa 96
 Tyr Gly Ser Gln Leu Ala Tyr Ala Asp Glu Asn Leu Lys Asp Leu Lys
 20 25 30

aga agt tta aga ttt gcc tat aat att acc cca tgc gat tat gaa aat 144
 Arg Ser Leu Arg Phe Ala Tyr Asn Ile Thr Pro Cys Asp Tyr Glu Asn
 35 40 45

gta gaa att gca ttt gtt act aca aat agc ata cat att aat act aaa 192
 Val Glu Ile Ala Phe Val Thr Thr Asn Ser Ile His Ile Asn Thr Lys
 50 55 60

caa aaa aga tcg gaa tgt att ctt tat gtt gat tct att gta tct tta Gln Lys Arg Ser Glu Cys Ile Leu Tyr Val Asp Ser Ile Val Ser Leu 65 70 75 80	240
ggc att act gat cag ttt ata aaa ggg gat aag gtc gat gtt ttt ggt Gly Ile Thr Asp Gln Phe Ile Lys Gly Asp Lys Val Asp Val Phe Gly 85 90 95	288
ctc cct tat aat ttt tcc cca cct tat gta gat aat att tat ggt ggt Leu Pro Tyr Asn Phe Ser Pro Pro Tyr Val Asp Asn Ile Tyr Gly Gly 100 105 110	336
att gta aaa cat tcg aat caa gga aat aaa tca tta cag ttt gta gga Ile Val Lys His Ser Asn Gln Gly Asn Lys Ser Leu Gln Phe Val Gly 115 120 125	384
att tta aat caa gat ggg aaa gaa act tat ttg ccc tct gag gct gtt Ile Leu Asn Gln Asp Gly Lys Glu Thr Tyr Leu Pro Ser Glu Ala Val 130 135 140	432
cgc ata aaa aag aaa cag ttt act tta cag gaa ttt gat ttt aaa ata Arg Ile Lys Lys Gln Phe Thr Leu Gln Glu Phe Asp Phe Lys Ile 145 150 155 160	480
aga aaa ttt cta atg gaa aaa tac aat atc tat gat tcg gaa tcg cgt Arg Lys Phe Leu Met Glu Lys Tyr Asn Ile Tyr Asp Ser Glu Ser Arg 165 170 175	528
tat aca tcg ggg agc ctt ttc ctt gct act aaa gat agt aaa cat tat Tyr Thr Ser Gly Ser Leu Phe Leu Ala Thr Lys Asp Ser Lys His Tyr 180 185 190	576
gaa gtt gat tta ttt aat aag gat gat aag ctt tta agt cga gac agt Glu Val Asp Leu Phe Asn Lys Asp Asp Lys Leu Leu Ser Arg Asp Ser 195 200 205	624
ttc ttt aaa agg tat aaa gat aat aag att ttt aat agt gaa gaa att Phe Phe Lys Arg Tyr Lys Asp Asn Lys Ile Phe Asn Ser Glu Glu Ile 210 215 220	672
agt cat ttt gat atc tac tta aaa acg cac tag Ser His Phe Asp Ile Tyr Leu Lys Thr His 225 230	705

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Arg Ser Leu Arg Phe Ala Tyr Asn Ile Thr Pro Cys Asp Tyr Glu Asn
 35 40 45

Val Glu Ile Ala Phe Val Thr Thr Asn Ser Ile His Ile Asn Thr Lys
 50 55 60

Gln Lys Arg Ser Glu Cys Ile Leu Tyr Val Asp Ser Ile Val Ser Leu
 65 70 75 80

Gly Ile Thr Asp Gln Phe Ile Lys Gly Asp Lys Val Asp Val Phe Gly
 85 90 95

Leu Pro Tyr Asn Phe Ser Pro Pro Tyr Val Asp Asn Ile Tyr Gly Gly
 100 105 110

Ile Val Lys His Ser Asn Gln Gly Asn Lys Ser Leu Gln Phe Val Gly
 115 120 125

Ile Leu Asn Gln Asp Gly Lys Glu Thr Tyr Leu Pro Ser Glu Ala Val
 130 135 140

Arg Ile Lys Lys Lys Gln Phe Thr Leu Gln Glu Phe Asp Phe Lys Ile
 145 150 155 160

Arg Lys Phe Leu Met Glu Lys Tyr Asn Ile Tyr Asp Ser Glu Ser Arg
 165 170 175

Tyr Thr Ser Gly Ser Leu Phe Leu Ala Thr Lys Asp Ser Lys His Tyr
 180 185 190

Glu Val Asp Leu Phe Asn Lys Asp Asp Lys Leu Leu Ser Arg Asp Ser
 195 200 205

Phe Phe Lys Arg Tyr Lys Asp Asn Lys Ile Phe Asn Ser Glu Glu Ile
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Ser His Phe Asp Ile Tyr Leu Lys Thr His
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 <213> Streptococcus pyogenes

<220>
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 Met Ile Ile Cys Leu Ser Phe Leu Leu Tyr Ser Asn Val Val Gln Ala
 20 25 30

aat tct tat aat aca acc aat aga cat aat cta gaa tcg ctt tat aag Asn Ser Tyr Asn Thr Thr Asn Arg His Asn Leu Glu Ser Leu Tyr Lys 35 40 45	144
cat gat tct aac ttg att gaa gcc gat agt ata aaa aat tct cca gat His Asp Ser Asn Leu Ile Glu Ala Asp Ser Ile Lys Asn Ser Pro Asp 50 55 60	192
att gta aca agc cat atg ttg aaa tat agt gtc aag gat aaa aat ttg Ile Val Thr Ser His Met Leu Lys Tyr Ser Val Lys Asp Lys Asn Leu 65 70 75 80	240
tca gtt ttt ttt gag aaa gat tgg ata tca cag gaa ttc aaa gat aaa Ser Val Phe Phe Glu Lys Asp Trp Ile Ser Gln Glu Phe Lys Asp Lys 85 90 95	288
gaa gta gat att tat gct cta tct gca caa gag gtt tgt gaa tgt cca Glu Val Asp Ile Tyr Ala Leu Ser Ala Gln Glu Val Cys Glu Cys Pro 100 105 110	336
ggg aaa agg tat gaa gcg ttt ggt gga att aca tta act aat tca gaa Gly Lys Arg Tyr Glu Ala Phe Gly Gly Ile Thr Leu Thr Asn Ser Glu 115 120 125	384
aaa aaa gaa att aaa gtt cct gta aac gtg tgg gat aaa agt aaa caa Lys Lys Glu Ile Lys Val Pro Val Asn Val Trp Asp Lys Ser Lys Gln 130 135 140	432
cag ccg cct atg ttt att aca gtc aat aaa ccg aaa gta acc gct cag Gln Pro Pro Met Phe Ile Thr Val Asn Lys Pro Lys Val Thr Ala Gln 145 150 155 160	480
gaa gtg gat ata aaa gtt aga aag tta ttg att aag aaa tac gat atc Glu Val Asp Ile Lys Val Arg Lys Leu Leu Ile Lys Lys Tyr Asp Ile 165 170 175	528
tat aat aac cgg gaa caa aaa tac tct aaa gga act gtt acc tta gat Tyr Asn Asn Arg Glu Gln Lys Tyr Ser Lys Gly Thr Val Thr Leu Asp 180 185 190	576
tta aat tca ggt aaa gat att gtt ttt gat ttg tat tat ttt ggc aat Leu Asn Ser Gly Lys Asp Ile Val Phe Asp Leu Tyr Tyr Phe Gly Asn 195 200 205	624
gga gac ttt aat agc atg cta aaa ata tat tcc aat aac gag aga ata Gly Asp Phe Asn Ser Met Leu Lys Ile Tyr Ser Asn Asn Glu Arg Ile 210 215 220	672
gac tca act caa ttt cat gta gat gtg tca atc agc taa Asp Ser Thr Gln Phe His Val Asp Val Ser Ile Ser 225 230 235	711
<210> 6	
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<213> Streptococcus pyogenes	

<400> 6

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				20				25				30			

Asn	Ser	Tyr	Asn	Thr	Thr	Asn	Arg	His	Asn	Leu	Glu	Ser	Leu	Tyr	Lys
				35			40				45				

His	Asp	Ser	Asn	Leu	Ile	Glu	Ala	Asp	Ser	Ile	Lys	Asn	Ser	Pro	Asp
				50			55			60					

Ile	Val	Thr	Ser	His	Met	Leu	Lys	Tyr	Ser	Val	Lys	Asp	Lys	Asn	Leu
				65		70			75		80				

Ser	Val	Phe	Phe	Glu	Lys	Asp	Trp	Ile	Ser	Gln	Glu	Phe	Lys	Asp	Lys
				85				90			95				

Glu	Val	Asp	Ile	Tyr	Ala	Leu	Ser	Ala	Gln	Glu	Val	Cys	Glu	Cys	Pro
				100			105			110					

Gly	Lys	Arg	Tyr	Glu	Ala	Phe	Gly	Gly	Ile	Thr	Leu	Thr	Asn	Ser	Glu
				115			120			125					

Lys	Lys	Glu	Ile	Lys	Val	Pro	Val	Asn	Val	Trp	Asp	Lys	Ser	Lys	Gln
				130		135			140						

Gln	Pro	Pro	Met	Phe	Ile	Thr	Val	Asn	Lys	Pro	Lys	Val	Thr	Ala	Gln
				145		150			155			160			

Glu	Val	Asp	Ile	Lys	Val	Arg	Lys	Leu	Leu	Ile	Lys	Lys	Tyr	Asp	Ile
				165			170			175					

Tyr	Asn	Asn	Arg	Glu	Gln	Lys	Tyr	Ser	Lys	Gly	Thr	Val	Thr	Leu	Asp
				180			185			190					

Leu	Asn	Ser	Gly	Lys	Asp	Ile	Val	Phe	Asp	Leu	Tyr	Tyr	Phe	Gly	Asn
				195			200			205					

Gly	Asp	Phe	Asn	Ser	Met	Leu	Lys	Ile	Tyr	Ser	Asn	Asn	Glu	Arg	Ile
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<211> 414

<212> DNA

<213> Streptococcus pyogenes

<220>

<221> CDS

<222> (1)...(411)

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gtt aca cca tca gta aac agt aat tcg gaa aat agt aaa att gta ggt 96
 Val Thr Pro Ser Val Asn Ser Asn Ser Glu Asn Ser Lys Ile Val Gly
 20 25 30

aat tta cta ata gat gga gtc cag caa aaa aca cta ata aat ccc ata 144
 Asn Leu Leu Ile Asp Gly Val Gln Gln Lys Thr Leu Ile Asn Pro Ile
 35 40 45

aaa ata gat aaa cct att ttt acg att caa gaa ttt gac ttc aaa atc 192
 Lys Ile Asp Lys Pro Ile Phe Thr Ile Gln Glu Phe Asp Phe Lys Ile
 50 55 60

aga caa tat ctt atg caa aca tac aaa att tat gat cct aat tct cca 240
 Arg Gln Tyr Leu Met Gln Thr Tyr Lys Ile Tyr Asp Pro Asn Ser Pro
 65 70 75 80

tac ata aaa ggg caa tta gaa att gcg atc aat ggc aat aaa cat gaa 288
 Tyr Ile Lys Gly Gln Leu Glu Ile Ala Ile Asn Gly Asn Lys His Glu
 85 90 95

agt ttt aac tta tat gat gca acc tca tct agt aca agg agt gat att 336
 Ser Phe Asn Leu Tyr Asp Ala Thr Ser Ser Ser Thr Arg Ser Asp Ile
 100 105 110

ttt aaa aaa tat aaa gac aat aag act ata aat atg aaa gat ttc agc 384
 Phe Lys Lys Tyr Lys Asp Asn Lys Thr Ile Asn Met Lys Asp Phe Ser
 115 120 125

cat ttt gat att tac ctt tgg act aaa taa 414
 His Phe Asp Ile Tyr Leu Trp Thr Lys
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<211> 137
<212> PRT
<213> Streptococcus pyogenes

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 20 25 30

Asn Leu Leu Ile Asp Gly Val Gln Gln Lys Thr Leu Ile Asn Pro Ile
 35 40 45

Lys Ile Asp Lys Pro Ile Phe Thr Ile Gln Glu Phe Asp Phe Lys Ile
 50 55 60

Arg Gln Tyr Leu Met Gln Thr Tyr Lys Ile Tyr Asp Pro Asn Ser Pro
 65 70 75 80

Tyr Ile Lys Gly Gln Leu Glu Ile Ala Ile Asn Gly Asn Lys His Glu
 85 90 95
 Ser Phe Asn Leu Tyr Asp Ala Thr Ser Ser Ser Thr Arg Ser Asp Ile
 100 105 110
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 115 120 125
 His Phe Asp Ile Tyr Leu Trp Thr Lys
 130 135

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 <211> 204
 <212> PRT
 <213> Streptococcus pyogenes

<400> 9
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 35 40 45
 Asn Ser Glu Met Asp Glu Tyr Ala Ala Asn Asp Phe Lys Asp Gly Asp
 50 55 60
 Lys Ile Ala Met Phe Ser Val Pro Phe Asp Trp Asn Tyr Leu Ser Glu
 65 70 75 80
 Gly Lys Val Ile Ala Tyr Thr Tyr Gly Met Thr Pro Tyr Gln Glu Glu
 85 90 95
 Pro Met Ser Lys Asn Ile Pro Val Leu Trp Ile Asn Arg Arg Gln Ile
 100 105 110
 Pro Val Pro Tyr Asn Gln Ile Ser Thr Asn Lys Thr Thr Val Thr Ala
 115 120 125
 Gln Glu Ile Asp Leu Lys Val Lys Phe Leu Ile Ser Gln His Gln Leu
 130 135 140
 Ser Ser Gly Ser Ser Tyr Lys Ser Gly Lys Leu Val Phe His Thr Asn
 145 150 155 160
 Asp Asn Ser Asp Lys Tyr Ser Leu Asp Leu Phe Tyr Val Gly Tyr Arg
 165 170 175
 Asp Lys Glu Ser Ile Phe Lys Val Tyr Lys Asp Lys Ser Phe Asn Ile
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Asp Lys Ile Gly His Leu Asp Ile Glu Ile Asp Ser
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 <212> PRT
 <213> Streptococcus pyogenes

<400> 10
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Tyr Thr Ile Thr Pro Tyr Asp Tyr Lys Asp Cys Arg Val Asn Phe Ser
 20 25 30

Thr Thr His Thr Leu Asn Ile Asp Thr Gln Lys Tyr Arg Gly Lys Asp
 35 40 45

Tyr Tyr Ile Ser Ser Glu Met Ser Tyr Glu Ala Ser Gln Lys Phe Lys
 50 55 60

Arg Asp Asp His Val Asp Val Phe Gly Leu Phe Tyr Ile Leu Asn Ser
 65 70 75 80

His Thr Gly Glu Tyr Ile Tyr Gly Ile Thr Pro Ala Gln Asn Asn Lys
 85 90 95

Val Asn His Lys Leu Leu Gly Leu Phe Ile Ser Gly Glu Ser Gln Gln
 100 105 110

Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys Asp Ile Val Thr Phe Gln
 115 120 125

Glu Ile Asp Phe Lys Ile Lys Tyr Leu Met Asp Asn Tyr Lys Ile Asp
 130 135 140

Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile Gly Thr Lys Asp
 145 150 155 160

Gly Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro Asn Glu Gly Thr
 165 170 175

Arg Ser Asp Ile Phe Ala Lys Tyr Lys Asp Arg Ile Ile Asn Met Lys
 180 185 190

Asn Phe Ser His Phe Asp Ile Tyr Leu Glu Lys
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 <212> PRT
 <213> Staphylococcus aureus

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 20 25 30

Glu Lys Ala Lys Thr Glu Asn Lys Glu Ser His Asp Gln Phe Leu Gln
 35 40 45

His Thr Ile Leu Phe Lys Gly Phe Phe Thr Asn His Ser Trp Tyr Asn
 50 55 60

Asp Leu Leu Val Asp Phe Asp Ser Lys Asp Ile Val Asp Lys Tyr Lys
 65 70 75 80

Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys Ala
 85 90 95

Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Val Thr Leu His
 100 105 110

Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn Leu Trp
 115 120 125

Leu Asp Lys Gln Asn Thr Val Pro Leu Glu Thr Val Lys Thr Asn Lys
 130 135 140

Lys Asn Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg Tyr Leu Gln
 145 150 155 160

Glu Lys Tyr Asn Leu Asn Ser Asp Val Phe Asp Gly Lys Val Gln Arg
 165 170 175

Gly Leu Ile Val Phe His Thr Ser Thr Glu Pro Ser Val Asn Tyr Asp
 180 185 190

Leu Phe Gly Ala Gln Gly Gln Asn Ser Asn Thr Leu Leu Arg Ile Tyr
 195 200 205

Arg Asp Lys Thr Ile Asn Ser Glu Asn Met His Ile Asp Ile Tyr Leu
 210 215 220

Tyr Thr Ser
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<210> 12
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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24

<210> 13
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<212> DNA		
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<223> Description of Artificial Sequence: Primer		
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<210> 14		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Primer		
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<210> 15		
<211> 21		
<212> DNA		
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<223> Description of Artificial Sequence: Primer		
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<210> 16		
<211> 26		
<212> DNA		
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<223> Description of Artificial Sequence: Primer		
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ttggatccaa ttcttataat acaacc		26
<210> 17		
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<223> Description of Artificial Sequence: Primer		
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aaaagctttt agctgattga cac		23

<210> 18
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<212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 18
gctatttcgg agagaaccag 20

<210> 19
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<223> Description of Artificial Sequence: Primer

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ctgaaacatc taagtagctg 20

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